

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (Currently Amended) A composition comprising a protein in crystalline form wherein the protein consists of residues 125-391 of SEQ ID NO:1, wherein said protein is in complex with an ATP-binding site ligand, and wherein the protein crystal has a crystal lattice in a $P6_122$ space group and unit cell dimensions, $\pm 5\%$, of $a=80.45\text{\AA}$, $b=80.45\text{\AA}$ and $c=172.18\text{\AA}$.
- 2-3. (Canceled)
4. (Previously Presented) The composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution of a value equal to or less than 3.0 Angstroms.
- 5-8. (Canceled)
9. (Currently Amended) A method for forming a crystal of a protein comprising:
forming a crystallization volume comprising a precipitant solution and a protein that consists of residues 125-391 of SEQ ID NO:1, wherein said protein is in complex with an ATP binding site ligand and wherein the protein crystal has a crystal lattice in a $P6_122$ space group and unit cell dimensions, $\pm 5\%$, of $a=80.45\text{\AA}$, $b=80.45\text{\AA}$ and $c=172.18\text{\AA}$; and
storing the crystallization volume under conditions suitable for crystal formation of the protein.
- 10-11. (Canceled)
12. (Previously Presented) The method according to claim 9 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution of a value equal to or less than 3.0 Angstroms.
- 13-14. (Canceled)

15. (Previously Presented) The method according to claim 9, wherein a protein crystal is formed, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.
16. (Canceled)
17. (Currently Amended) A non-crystalline protein consisting of SEQ ID NO:3.
18. (Withdrawn) A method of identifying an entity that associates with a protein comprising:
taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ ID NO:3, and wherein the protein crystal has a crystal lattice in a P6₁22 space group and unit cell dimensions, +/-5%, of a=80.45Å, b=80.45Å and c=172.18Å; and
performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.
- 19-21. (Canceled)
22. (Withdrawn) A method according to claim 18, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.
23. (Withdrawn) A method according to claim 18, the method further comprising measuring an activity of the protein when contacted with the one or more entities.
24. (Withdrawn) A method according to claim 18, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present.
25. (Withdrawn) A method according to claim 18, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.

26. (Canceled)
27. (Previously Presented) The method according to claim 15, the method further comprising:
performing rational drug design using the solved structure; and
identifying an entity that associates with the protein.
28. (Previously Presented) The method according to claim 27 further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.
29. (Previously Presented) The method according to claim 27 further comprising measuring an activity of the protein when contacted with the one or more entities.
30. (Currently Amended) A non-crystalline protein consisting of residues 125-391 of SEQ ID NO:1.
31. (Currently Amended) A non-crystalline protein consisting of residues 24-295 of SEQ ID NO:3.
32. (Currently Amended) A composition comprising a protein in crystalline form wherein the protein consists of residues 24-295 of SEQ ID NO:3, wherein said protein is in complex with an ATP binding site ligand and wherein the protein crystal has a crystal lattice in a P6₁22 space group and unit cell dimensions, +/-5%, of a=80.45Å, b=80.45Å and c=172.18Å.
33. (Currently Amended) A method for forming a crystal of a protein comprising:
forming a crystallization volume comprising a precipitant solution and a protein that consists of residues 24-295 of SEQ ID NO:3, wherein said protein is in complex with an ATP binding site ligand and wherein the protein crystal has a crystal lattice in a P6₁22 space group and unit cell dimensions, +/-5%, of a=80.45Å, b=80.45Å and c=172.18Å; and
storing the crystallization volume under conditions suitable for crystal formation of the protein.
34. (New) An isolated non-crystalline protein consisting of residues 24-295 of SEQ ID NO:3.
35. (New) An isolated non-crystalline protein consisting of residues 125-391 of SEQ ID NO:1.
36. (New) An isolated non-crystalline protein consisting of SEQ ID NO:3.